We have analysed all 40 notochord cells in 5 embryos at each of 9 time points over a three hour period starting at the end of notochord cell intercalation. The notochord cells are roughly cylindrical over this period, but change their aspect ratio from disk-shaped to barrel-shaped as the tail elongates. We find that anterior-posterior position in the notochord has a major influence on notochord cell shape, with cells being tallest at the front of the notochord but widest in the middle. These differences are largely persistent over time, but do not correspond to the primary versus secondary notochord lineages, suggesting that they may be mechanical in origin. The notochord cell aspect ratio change is initially characterized by a dramatic decrease in anterior and posterior surface area, while lateral surface area remains relatively constant. Pharmacological inhibitors of both actomysosin-dependent contractility and endocytosis inhibit the AP surface area decrease. We are currently confirming the importance of contractility and endocytosis by transgenesis of relevant reporter and dominant-negative constructs.

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Program/Abstract # 122
Sexual Dimorphism of the adult Drosophila abdomen: Wingless, segmental fusion and fate transformation
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A striking sexual dimorphism of adult Drosophilia is a difference in overt segmentation. Females developseven abdominal segments and males only six. The posterior-most female segment (A7)is modified with respect to more anterior segments, while male A7 is absent, presumably fused to its anterior neighbor, A6. This trait is likelysynapomorphic to higher diptera (Brachycera) as male reduction and femalemodifications to posterior segments occur throughout this clade; segment numberis monomorphic in lower diptera. We are investigating the genetic basis of thistrait in Drosophila to gain insightinto mechanisms of sexual dimorphism and the evolution of complex morphologicaltraits. Our current aims address the fate of male A7. Adult abdominal segmentsdevelop from histoblast cells specified during embryogenesis. Developmentaltime-course analyses showed male A7 histoblasts are established and do proliferateduring pupation. However, during pupal development anterior male A7 cellsdisappear. The anterior A7 compartment is void of cells by 42 hours APF, asvisualized by the posterior compartment marker Engrailed. Male-specific A7 apoptosis is not observed, suggesting anterior male A7cells either migrate from the epithelium or are transformed, being absorbed bythe more anterior A6 cells. We found the morphogen wingless is specificallyabsent from pupal male A7. The necessity of wingless to specify adult abdominalcell fate has previously been shown (Shirras and Couso, 1996). We will present data that in theabsence of Wg, anterior male A6 cells are transformed to posterior identity,being absorbed by the more anterior segment A6.

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Program/Abstract # 123
Activin signaling is required for Drosophila follicle cell development and normal female fertility
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The *Drosophila* Activin signaling is initiated by Activin-type ligand Activin-β or Activin-like protein Dawdle, either of which can bind type I receptor Babo and type II receptor Punt leading to the phosphorylation of the cytoplasmic protein Smad2. This signaling event has previously been shown to regulate different aspects of neurogenesis and axon guidance. Here we demonstrate that the two ligands Activin-β and Dawdle are expressed in developing follicle cells in oogenesis, and that both ligands are required for regulating normal follicle cell adhesions. We also found that Smad2 is not only required for regulating follicle cell adhesions but also for maintaining normal follicle cell size and shape. Without Activin or Activin-like signaling, *Activin-β* mutant, *Dawdle* mutant, and Smad2 knock-down females showed severe fertility problems. These females ceased to produce mature eggs at their very early ages after they hatched from pupae. Our data demonstrate that Activin signaling plays an important role in normal *Drosophila* follicle cell development and in normal *Drosophila* female fertility regulation.

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Program/Abstract # 124
Glia influence patterning of adult muscle innervation in Drosophila
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The stereotypy of DLM innervation lies in the number of contact points (CPs) made by each motor neuron and is established as a consequence of pruning that occurs during metamorphosis. On the dorsal most DLM fiber, 5 contact points are usually seen (n=13). We disrupted adult-specific glial ensheathment using a targeted expression of dominant negative shibire. This manipulation resulted in fewer contact points at the DLM fibers (3.7 ± 0.23; n=9). Our studies suggest that glial-neuronal interactions, specifically during pruning are important for the patterning of adult innervation.At the end of the pruning phase, FasII localizes to glia, which envelops each of the stabilized contact points. When glial FasII levels are increased using the Gal4/UAS system of targeted expression, pruning of secondary branches is enhanced (4.6 ± 0.17; n=19). Our results indicate that glia regulate pruning of secondary branches by influencing the balance between stabilization and pruning. This was confirmed by an observed rescue of the innervation phenotype of FasII hypomorphs by over expressing FasII in glia.

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Program/Abstract # 125
The role of post-transcriptional gene regulation in dendritic morphogenesis
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Neurons have an asymmetric cellular morphology that translates into polarized cellular functions necessary for establishing neural circuitry. While the mechanisms for establishing neuronal polarity are poorly understood, it is well established that mechanisms that generate asymmetric protein distributions are essential for such cellular polarity at the morphological and functional levels. In neurons, mRNA localization and translational repression are used to change the protein composition of various regions of the cell, allowing for distinct axonal and dendritic morphologies and environments. A significant portion of eukaryotic genomes encode for RNA-binding proteins and other components of post-transcriptional regulatory machinery. Moreover, many mRNAs are